



*Mci*

PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/019,368

DATE: 08/05/2005  
TIME: 11:04:30

Input Set : A:\pto.da.txt  
Output Set: N:\CRP4\08042005\J019368.raw

4 <110> APPLICANT: Dean, Nicholas M.  
 5 ISIS PHARMACEUTICALS, INC.  
 7 <120> TITLE OF INVENTION: Antisense Oligonucleotide Modulation of Human Protein  
 8 Kinase C-delta Expression  
 10 <130> FILE REFERENCE: ISPH-0458  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/019,368  
 C--> 12 <141> CURRENT FILING DATE: 2001-11-13  
 12 <150> PRIOR APPLICATION NUMBER: 1999-05-18  
 W--> 13 <151> PRIOR FILING DATE: US 09/313,930  
 15 <160> NUMBER OF SEQ ID NOS: 20  
 17 <170> SOFTWARE: PatentIn Ver. 2.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 2104  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (59)..(2089)  
 28 <300> PUBLICATION INFORMATION:  
 29 <301> AUTHORS: Aris, J . P.  
 30 Basta, P. V.  
 31 Holmes, W. D.  
 32 Ballas, L. M.  
 33 Moomaw, C.  
 34 Rankl, N. B.  
 35 Blobel, G.  
 36 Loomis, C. R.  
 37 Burns, D. J.  
 38 <302> TITLE: Molecular and biochemical characterization of a  
 39 recombinant human PKC-delta family member  
 40 <303> JOURNAL: Biochim. Biophys. Acta  
 41 <304> VOLUME: 1174  
 42 <305> ISSUE: 2  
 43 <306> PAGES: 171-181  
 44 <307> DATE: 1993-08-19  
 45 <308> DATABASE ACCESSION NO: L07860  
 46 <309> DATABASE ENTRY DATE: 1993-11-02  
 48 <400> SEQUENCE: 1  
 49 tgccggcgcc acccttggcg cctgccccctg caacgggagc cccactgcag gccccacc 58  
 51 atg gcg ccg ttc ctg cgc atc gcc ttc aac tcc tat gag ctg ggc tcc 106  
 52 Met Ala Pro Phe Leu Arg Ile Ala Phe Asn Ser Tyr Glu Leu Gly Ser  
 53 1 5 10 15  
 55 ctg cag gcc gag gac gag gcg aac cag ccc ttc tgt gcc gtg aag atg 154

*Does Not Comply*  
*Corrected Diskette Needed*  
*(PS,1)*

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56	Leu Gln Ala Glu Asp Glu Ala Asn Gln Pro Phe Cys Ala Val Lys Met			
57	20	25	30	
59	aag gag gcg ctc agc aca gag cgt ggg aaa aca ctg gtg cag aag aag	202		
60	Lys Glu Ala Leu Ser Thr Glu Arg Gly Lys Thr Leu Val Gln Lys Lys			
61	35	40	45	
63	ccg acc atg tat cct gag tgg aag tcg acg ttc gat gcc cac atc tat	250		
64	Pro Thr Met Tyr Pro Glu Trp Lys Ser Thr Phe Asp Ala His Ile Tyr			
65	50	55	60	
67	gag ggg cgc gtc atc cag att gtg cta atg cgg gca gca gag gag cca	298		
68	Glu Gly Arg Val Ile Gln Ile Val Leu Met Arg Ala Ala Glu Glu Pro			
69	65	70	75	80
71	gtg tct gag gtg acc gtt gtg tgg ctg gtc gag cgc tgc aag	346		
72	Val Ser Glu Val Thr Val Gly Val Ser Val Leu Ala Glu Arg Cys Lys			
73	85	90	95	
75	aag aac aat ggc aag gct gag ttc tgg ctg gac ctg cag cct cag gcc	394		
76	Lys Asn Asn Gly Lys Ala Glu Phe Trp Leu Asp Leu Gln Pro Gln Ala			
77	100	105	110	
79	aag gtg ttg atg tct gtt cag tat ttc ctg gag gac gtg gat tgc aaa	442		
80	Lys Val Leu Met Ser Val Gln Tyr Phe Leu Glu Asp Val Asp Cys Lys			
81	115	120	125	
83	caa tct atg cgc agt gag gac gag gcc aag ttc cca acg atg aac cgc	490		
84	Gln Ser Met Arg Ser Glu Asp Glu Ala Lys Phe Pro Thr Met Asn Arg			
85	130	135	140	
87	cgc gga gcc atc aaa cag gcc aaa atc cac tac atc aag aac cat gag	538		
88	Arg Gly Ala Ile Lys Gln Ala Lys Ile His Tyr Ile Lys Asn His Glu			
89	145	150	155	160
91	ttt atc gcc acc ttc ttt ggg caa ccc acc ttc tgt tct gtg tgc aaa	586		
92	Phe Ile Ala Thr Phe Phe Gly Gln Pro Thr Phe Cys Ser Val Cys Lys			
93	165	170	175	
95	gac ttt gtc tgg ggc ctc aac aag caa ggc tac aaa tgc agg caa tgt	634		
96	Asp Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Lys Cys Arg Gln Cys			
97	180	185	190	
99	aac gct gcc atc cac aag aaa tgc atc gac aag atc atc ggc aga tgc	682		
100	Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Ile Ile Gly Arg Cys			
101	195	200	205	
103	act ggc acc gcg gcc aac agc cgg gac act ata ttc cag aaa gaa cgc	730		
104	Thr Gly Thr Ala Ala Asn Ser Arg Asp Thr Ile Phe Gln Lys Glu Arg			
105	210	215	220	
107	ttc aac atc gac atg cgg cac cgc ttc aag gtt cac aac tac atg agc	778		
108	Phe Asn Ile Asp Met Pro His Arg Phe Lys Val His Asn Tyr Met Ser			
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111	ccc acc ttc tgt gac cac tgc ggc agc ctg ctc tgg gga ctg gtg aag	826		
112	Pro Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Leu Val Lys			
113	245	250	255	
115	cag gga tta aag tgt gaa gac tgc ggc atg aat gtg cac cat aaa tgc	874		
116	Gln Gly Leu Lys Cys Glu Asp Cys Gly Met Asn Val His His Lys Cys			
117	260	265	270	
119	cgg gag aag gtg gcc aac ctc tgc ggc atc eac cag aag ctt ttg gct	922		
120	Arg Glu Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Leu Ala			

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123	gag gcc ttg aac caa gtc acc cag aga gcc tcc cggtt	aga tca gac tca		970
124	Glu Ala Leu Asn Gln Val Thr Gln Arg Ala Ser Arg Arg Ser Asp Ser			
125	290	295	300	
127	gcc tcc tca gag cct gtt ggg ata tat cag ggt ttc gag aag aag acc			1018
128	Ala Ser Ser Glu Pro Val Gly Ile Tyr Gln Gly Phe Glu Lys Lys Thr			
129	305	310	315	320
131	gga gtt gct ggg gag gac atg caa gac aac agt ggg acc tac ggc aag			1066
132	Gly Val Ala Gly Glu Asp Met Gln Asp Asn Ser Gly Thr Tyr Gly Lys			
133	325	330	335	
135	atc tgg gag ggc agc agc aag tgc aac atc aac ttc atc ttc cac			1114
136	Ile Trp Glu Gly Ser Ser Lys Cys Asn Ile Asn Asn Phe Ile Phe His			
137	340	345	350	
139	aag gtc ctg ggc aaa ggc agc ttc ggg aag gtg ctg ctt gga gag ctg			1162
140	Lys Val Leu Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Gly Glu Leu			
141	355	360	365	
143	aag ggc aga gga gag tac tct gcc atc aag gcc ctc aag aag gat gtg			1210
144	Lys Gly Arg Gly Glu Tyr Ser Ala Ile Lys Ala Leu Lys Lys Asp Val			
145	370	375	380	
147	gtc ctg atc gac gac gac gtg gag tgc acc atg gtt gag aag cgg gtg			1258
148	Val Leu Ile Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val			
149	385	390	395	400
151	ctg aca ctt gcc gca gag aat ccc ttt ctc acc cac ctc atc tgc acc			1306
152	Leu Thr Leu Ala Ala Glu Asn Pro Phe Leu Thr His Leu Ile Cys Thr			
153	405	410	415	
155	ttc cag acc aag gac cac ctg ttc ttt gtg atg gag ttc ctc aac ggg			1354
156	Phe Gln Thr Lys Asp His Leu Phe Phe Val Met Glu Phe Leu Asn Gly			
157	420	425	430	
159	ggg gac ctg atg tac cac atc cag gac aaa ggc cgc ttt gaa ctc tac			1402
160	Gly Asp Leu Met Tyr His Ile Gln Asp Lys Gly Arg Phe Glu Leu Tyr			
161	435	440	445	
163	cgt gcc acg ttt tat gcc gct gag ata atg tgt gga ctg cag ttt cta			1450
164	Arg Ala Thr Phe Tyr Ala Ala Glu Ile Met Cys Gly Leu Gln Phe Leu			
165	450	455	460	
167	cac agc aag ggc atc att tac agg gac ctc aaa ctg gac aat gtg ctg			1498
168	His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu			
169	465	470	475	480
171	ttg gac cgg gat ggc cac atc aag att gcc gac ttt ggg atg tgc aaa			1546
172	Leu Asp Arg Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys			
173	485	490	495	
175	gag aac ata ttc ggg gag agc cgg gcc agc acc ttc tgc ggc acc cct			1594
176	Glu Asn Ile Phe Gly Glu Ser Arg Ala Ser Thr Phe Cys Gly Thr Pro			
177	500	505	510	
179	gac tat atc gcc cct gag atc cta cag ggc ctg aag tac aca ttc tct			1642
180	Asp Tyr Ile Ala Pro Glu Ile Leu Gln Gly Leu Lys Tyr Thr Phe Ser			
181	515	520	525	
183	gtg gac tgg tgg tct ttc ggg gtc ctt ctg tac gag atg ctc att ggc			1690
184	Val Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu Ile Gly			
185	530	535	540	

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187	cag tcc ccc ttc cat ggt gat gat gag gat gaa ctc ttc gag tcc atc	1738
188	Gln Ser Pro Phe His Gly Asp Asp Glu Asp Glu Leu Phe Glu Ser Ile	
189	545 550 555 560	
191	cgt gtg gac acg cca cat tat ccc cgc tgg atc acc aag gag tcc aag	1786
192	Arg Val Asp Thr Pro His Tyr Pro Arg Trp Ile Thr Lys Glu Ser Lys	
193	565 570 575	
195	gac atc ctg gag aag ctc ttt gaa agg gaa cca acc aag agg ctg gga	1834
196	Asp Ile Leu Glu Leu Phe Glu Arg Glu Pro Thr Lys Arg Leu Gly	
197	580 585 590	
199	atg acg gga eac atc aaa atc cac ccc ttc aag acc ata aac tgg	1882
200	Met Thr Gly Asn Ile Lys Ile His Pro Phe Phe Lys Thr Ile Asn Trp	
201	595 600 605	
203	act ctg ctg gaa aag cgg agg ttg gag cca ccc ttc agg ccc aaa gtg	1930
204	Thr Leu Leu Glu Lys Arg Arg Leu Glu Pro Pro Phe Arg Pro Lys Val	
205	610 615 620	
207	aag tca ccc aga gac tac agt aac ttt gac cag gag ttc ctg aac gag	1978
208	Lys Ser Pro Arg Asp Tyr Ser Asn Phe Asp Gln Glu Phe Leu Asn Glu	
209	625 630 635 640	
211	aag gcg cgc ctc tcc tac agc gac aag aac ctc atc gac tcc atg gac	2026
212	Lys Ala Arg Leu Ser Tyr Ser Asp Lys Asn Leu Ile Asp Ser Met Asp	
213	645 650 655	
215	cag tct gca ttc gct ggc ttc tcc ttt gtg aac ccc aaa ttc gag cac	2074
216	Gln Ser Ala Phe Ala Gly Phe Ser Phe Val Asn Pro Lys Phe Glu His	
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227	<213> ORGANISM: Homo sapiens	
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234	20 25 30	
236	Lys Glu Ala Leu Ser Thr Glu Arg Gly Lys Thr Leu Val Gln Lys Lys	
237	35 40 45	
239	Pro Thr Met Tyr Pro Glu Trp Lys Ser Thr Phe Asp Ala His Ile Tyr	
240	50 55 60	
242	Glu Gly Arg Val Ile Gln Ile Val Leu Met Arg Ala Ala Glu Glu Pro	
243	65 70 75 80	
245	Val Ser Glu Val Thr Val Gly Val Ser Val Leu Ala Glu Arg Cys Lys	
246	85 90 95	
248	Lys Asn Asn Gly Lys Ala Glu Phe Trp Leu Asp Leu Gln Pro Gln Ala	
249	100 105 110	
251	Lys Val Leu Met Ser Val Gln Tyr Phe Leu Glu Asp Val Asp Cys Lys	
252	115 120 125	
254	Gln Ser Met Arg Ser Glu Asp Glu Ala Lys Phe Pro Thr Met Asn Arg	

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255	130	135	140
257	Arg Gly Ala Ile Lys Gln Ala Lys Ile His Tyr Ile Lys Asn His Glu		
258	145	150	155
260	Phe Ile Ala Thr Phe Phe Gly Gln Pro Thr Phe Cys Ser Val Cys Lys		160
261	165	170	175
263	Asp Phe Val Trp Gly Leu Asn Lys Gln Gly Tyr Lys Cys Arg Gln Cys		
264	180	185	190
266	Asn Ala Ala Ile His Lys Lys Cys Ile Asp Lys Ile Ile Gly Arg Cys		
267	195	200	205
269	Thr Gly Thr Ala Ala Asn Ser Arg Asp Thr Ile Phe Gln Lys Glu Arg		
270	210	215	220
272	Phe Asn Ile Asp Met Pro His Arg Phe Lys Val His Asn Tyr Met Ser		
273	225	230	235
275	Pro Thr Phe Cys Asp His Cys Gly Ser Leu Leu Trp Gly Leu Val Lys		240
276	245	250	255
278	Gln Gly Leu Lys Cys Glu Asp Cys Gly Met Asn Val His His Lys Cys		
279	260	265	270
281	Arg Glu Lys Val Ala Asn Leu Cys Gly Ile Asn Gln Lys Leu Leu Ala		
282	275	280	285
284	Glu Ala Leu Asn Gln Val Thr Gln Arg Ala Ser Arg Arg Ser Asp Ser		
285	290	295	300
287	Ala Ser Ser Glu Pro Val Gly Ile Tyr Gln Gly Phe Glu Lys Lys Thr		
288	305	310	315
290	Gly Val Ala Gly Glu Asp Met Gln Asp Asn Ser Gly Thr Tyr Gly Lys		320
291	325	330	335
293	Ile Trp Glu Gly Ser Ser Lys Cys Asn Ile Asn Asn Phe Ile Phe His		
294	340	345	350
296	Lys Val Leu Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Gly Glu Leu		
297	355	360	365
299	Lys Gly Arg Gly Glu Tyr Ser Ala Ile Lys Ala Leu Lys Lys Asp Val		
300	370	375	380
302	Val Leu Ile Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val		
303	385	390	395
305	Leu Thr Leu Ala Ala Glu Asn Pro Phe Leu Thr His Leu Ile Cys Thr		400
306	405	410	415
308	Phe Gln Thr Lys Asp His Leu Phe Phe Val Met Glu Phe Leu Asn Gly		
309	420	425	430
311	Gly Asp Leu Met Tyr His Ile Gln Asp Lys Gly Arg Phe Glu Leu Tyr		
312	435	440	445
314	Arg Ala Thr Phe Tyr Ala Ala Glu Ile Met Cys Gly Leu Gln Phe Leu		
315	450	455	460
317	His Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu		
318	465	470	475
320	Leu Asp Arg Asp Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys		480
321	485	490	495
323	Glu Asn Ile Phe Gly Glu Ser Arg Ala Ser Thr Phe Cys Gly Thr Pro		
324	500	505	510
326	Asp Tyr Ile Ala Pro Glu Ile Leu Gln Gly Leu Lys Tyr Thr Phe Ser		
327	515	520	525

08/05/05 FRI 11:19 FAX 703 308 4221

PTO/STIC

4015

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**VERIFICATION SUMMARY**

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DATE: 08/05/2005

TIME: 11:04:31

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\08042005\J019368.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD